

Figure 1A

Muc1 Exemplary Protein – (SEQ ID NO:19)

Signal Peptide Cleavage (G|S; A|S)

↓ ↓

1 MTPGTQSPFF LLLLLTLTV VTGSGHASST PGGEKETSAT QRSSVPSSTE KNAVSMTSSV LSSHSPGSGS

71 STTQGQDVTL APATEPASGS AATWGQDVTS VPVTRPALGS TTPPAHDVTS APDNKPAPGS TAPPAHGVTS

141 APDTRPPPGS TAPPAHGVTS APDTRPPPGS TAPAAHGVTS APDTRPAPGS TAPPAHGVTS APDNRPALAS

211 TAPPVHNVT ASGSASGSAS TLVHNGTSAR ATTPASKST PFSIPSHSD TPTTLASHST KTDASSTHHS

281 TVPPLTSSNH STSPQLSTGV SFFFLSFHIS NLQFNSSLED PSTDYQELQ RDISEMFLQI YKQGGFLGLS

Post-translational cleavage site (G|S)

↓

351 NIKFRPGSVV VQLTLAFREG TINVHDVETQ FNQYKTEAAS RYNLTISDVS VSDVPPFSA QSGAGVPGWG

421 IALLVLVCL VALAIVYLIA LAVCQCRKN YQLDIFPAR DTYHPMSEYP TYTHGRYVP PSSTDSPYE

Transmembrane region (TMR)

491 KVSAGNGGSS LSYTNPAVAA TSANL (SEQ ID NO:19; NM_002456)

Figure 1B

<u>Muc1 juxtamembrane domain-GST Fusion</u>		
GST plus amino acids 337-422 of Muc1		
GST-FLQI YKQGGFLGLS NIKFRPGSVV VQLTLAFREG TINVHDVETQ FNQYKTEAAS RYNLTISDVS VSDVPPFFSA		
QSGAGVPGWG IA (SEQ ID NO:7)		
<u>Synthetic Peptides</u>		
Peptide a	21 amino acids (362-382)	QLTLAFREGTINVHDVETQFN (SEQ ID NO:8)
Peptide b	21 amino acids (383-403)	QYKTEAASRYNLTISDVSVD (SEQ ID NO:9)
Peptide c	21 amino acids (337-357)	FLQIYKQGGFLGLSNIKFRPG (SEQ ID NO:10)
Peptide d	21 amino acids (354-374)	FRPGSVVQLTLAFREGTINV (SEQ ID NO:11)
Peptide e	19 amino acids (404-422)	VPPFFSAQSGAGVPGWGIA (SEQ ID NO:12)

Figure 2A

Muc16 Exemplary Protein – (SEQ ID NO:20)

1	MEHITKIPNE	AAHRGTIRPV	KGPQTSTSPA	SPKGLHTGGT	KRMETTTTAL	KTTTALKTT	SRAITLTSVY	TPTLGLTLP	AMINO
81	NASRQMASTI	LTEMMITTPY	VFPDVPETTS	SLATSLGAET	STALPRTTPS	VLNRESETTA	SLVSRGAER	SPVIQTLDVS	TERMINAL
161	SSEPDTTASW	VIHPAETIPT	VSKTTPNFFH	SELDTVSSSTA	TSHGADVSSA	IPTNISPSEL	DALTPLVTIS	GTDTSFTFT	DOMAIN
241	LTKSPHETET	RTTWLTHPAE	TSSTIPRTIP	NFSHHESDAT	PSIATSPGAE	TSSAIPIMTV	SPGAEDLVTS	QVTSSGTDNRN	
321	MTIPTLTLS	GEPKTIASLV	THPEAQTS	IPSTTISPAV	SRLVTSMTVS	LAAKTSTTNR	ALTNSPGEPA	TTVSLVTHPA	
401	QTSPTVPWTT	SIFPHSKSDT	TPSMTTSHGA	ESSSAVPTPT	VSTEVPGVVT	PLVTSSRAVI	STTIPIILTL	PGEPEPTPSM	
481	ATSHGEEASS	AIPTPTVSPG	VPGVVTSLVT	SSRAVTSTTI	PILTFSLGEP	ETTPSMATSH	GTEAGSAVPT	VLPEVPGMVT	
561	SLVASSRAVT	STTLPTLTLS	PGEPEPTPSM	ATSHGAEASS	TVPTVSPEVP	GVVTSLVTS	SGVNSTSIPT	LILSPGELET	
641	TPSMATSHGA	EASSAVPTPT	VSPGVSGVVT	PLVTSSRAVT	STTIPIILTL	SSEPETTPSM	ATSHGVEASS	AVLTVSPEVP	
721	GMVTSLVTS	RAVTSSTIPT	LTISSDEPET	TTSLVTHSEA	KMISAIPTLA	VSPTVQGLVT	SLVTS	SSGSET	SAFSNLTVAS
801	SQPETIDSWV	AHPGTEASSV	VPTLT	VSTGE	PFTNISLVTH	TTSRFSHSEL	DTMPSTVTSP	EAESSAIST	
881	TISPGIPGVL	TSLVTSSGRD	ISATFPTVPE	SPHESEATAS	WVTHPAVTST	TVPR	TTPNYS	HSEPD	TTPSI
961	DFPTITVSPD	VPDMVTSQVT	SSGTDTSITI	PTLTLSGEP	ETTTSFITYS	ETHTSSAAPT	LPVSPGASKM	LTS	LVISSGT
1041	DSTTTTFTLT	ETPYEPTTA	IQLIHPAETN	TMVPKTTPKF	SHSKSDTTL	VAITSPGPEA	SSAVSTTTIS	PDMSDLVTSL	
1121	VPSSGTDST	TFPTLSETPY	EPETTVTWLT	HPAETSTTVS	GTIPNFSHRG	SDTAPSMVTS	PGVDTRSGVP	TTTIPPSIPG	
1201	VVTSQVTSSA	TDTSTAIPTL	TPSPGEPETT	ASSATHPGTQ	TGFTVPIRTV	PSSEPD	TMAS	WVTHPPQ	TST
1281	HSSPDATPVM	ATSPRTEASS	AVLT	TISPGA	PEMVTSQITS	TLTHSPG	MP	ET	TGTSKTFPAS
1361	TVFPQVSETT	ASLTIRPGAE	TSTALPTQTT	SSLFTLLVTG	TSRVDLSPTA	SPGVS	AKTAP	LSTHPGTETS	TMIPTSTLSL
1441	GLLETTGLLA	TSSSAETSTS	TLTLTVSPAV	SGLSSASITT	DKPQT	VT	TSWN	GPPEFSRTVT	GTTMTLIPSE
1521	MPTPKTSHG	EGVSPTTILR	TTMVEATNLA	TTGSSPTVAK	TTTTFTNTLAG	SLFTPL	TTPG	MSTLASESVT	SRTSYNHRSW
1601	ISTTSSYNRR	YWTPATSTPV	TSTFSPGIST	SSIPSSSTA					
1681	LKPLFRNSSL	EYLYSGCRLA	SLRPEKDSSA	MAVDAICTHR	AT	VPFMV	PFTLN	FTITNLQYEE	DMRHPGSRKF
1761	GFTHRSSMPT	TSTPGTSTVD	VGTS	GPSSS	PSPTAAGPLL	MPFTLNFTIT	NLQYEE	DMRR	TNGIQELGPY
1841	FKNTSVGPLY	SGCRLTLRLP	EKDGAA	TGVD	AICTHRLDPK	SPGLN	REQLY	WELSKLTNDI	EELGPYT
1921	QSSVSTTSTP	GTSTVDLRTS	GT	PSSLSSTP/-/					NSLYVNGFTH
11511	TYQLVDIHVT	EMESSVYQPT	SSSSTQHFPY	NFTITNLPYS	QDKAQPGTTN	YQNRKNRIED	ALNQLFRNSS	IKSYFSDCQV	CARBOXY
11591	STFRSVPNRH	HTGVDSLCNF	SPLARRVDRV	AIYEEFLRMT	RNGTQLQNF	LDRSSVLVDG	YSPNRNEPLT	GNSDLPFWAV	TERMINAL
11671	<u>ILIGLAGLIG</u>	<u>LITCLICGVL</u>	<u>VTTRRRKKEG</u>	<u>EYNVQQQCPG</u>	<u>YYQSHLDLED</u>	<u>LQ</u>			DOMAIN

Figure 2B

<u>Muc16 juxtamembrane domain-GST Fusion</u>				
GST plus amino acids 11559-11666 of Muc16				
GST-TN YQNRKNIED ALNQLFRNSS IKSYFSDCQV STFRSVPNRH HTGVDSL CNF SPLARRVDRV AIYEEFLRMT RNGTQLQNFT LDRSSVLVDG YSPNRNEPLT GNSDLP (SEQ ID NO:13)				
<u>Synthetic Peptides</u>				
Peptide a	20 amino acids	(11644-11663)	SSVLVDG YSPNRNEPLT GNS	(SEQ ID NO:14)
Peptide b	20 amino acids	(11559-11578)	TN YQNRKNIED ALNQLFRN	(SEQ ID NO:15)
Peptide c	21 amino acids	(11576-11596)	FRNSS IKSYFSDCQV STFRSV	(SEQ ID NO:16)
Peptide d	23 amino acids	(11595-11617)	SVPNRH HTGVDSL CNF SPLARRV	(SEQ ID NO:17)
Peptide e	28 amino acids	(11618-11645)	DRV AIYEEFLRMT RNGTQLQNFT LDRSS	(SEQ ID NO:18)

Figure 3

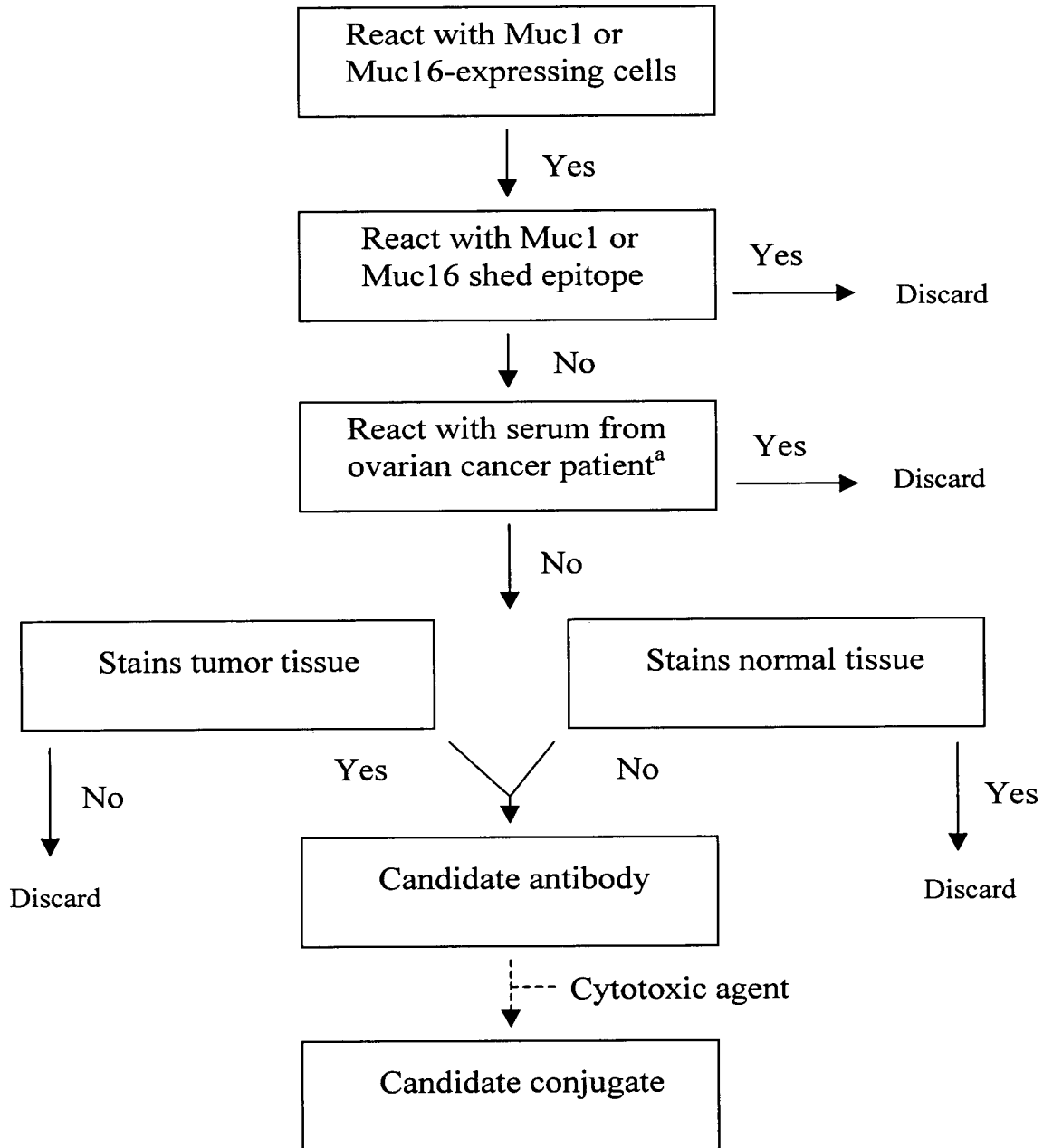
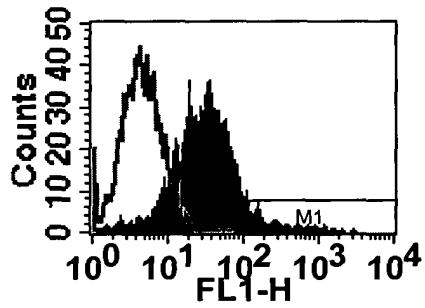
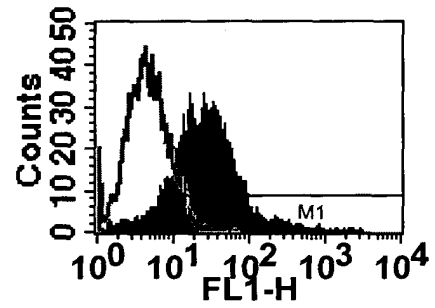


Figure 4A

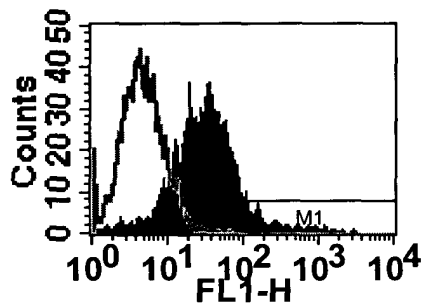
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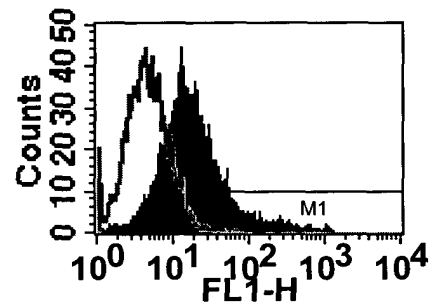
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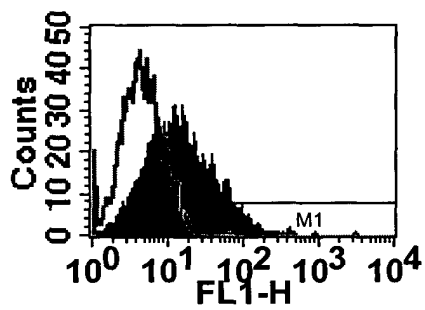
Clone 4H2



Clone 6H6



Clone 9B9



Clone 8H1

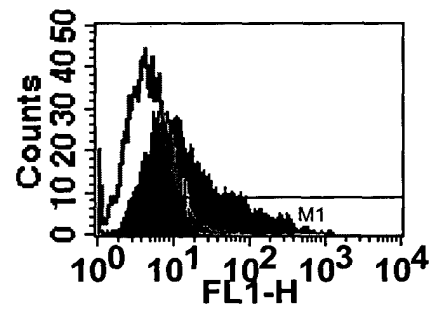
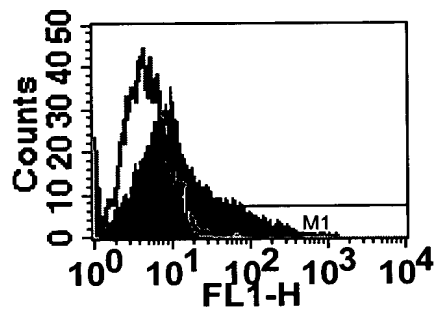
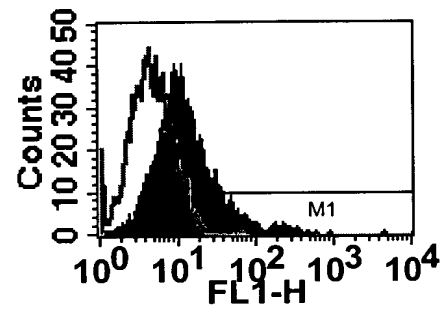


Figure 4A (continued)

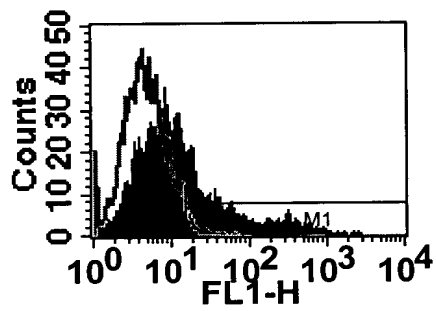
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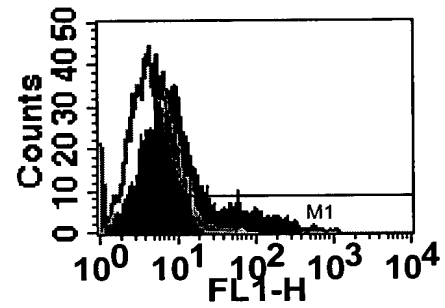
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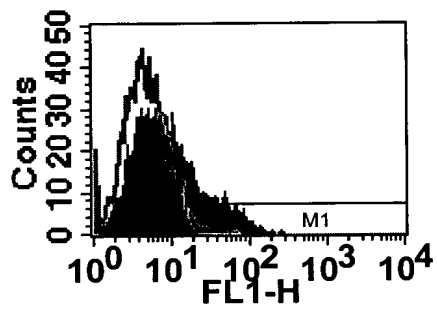
Clone 6C7



Clone 2A10



Clone 3A3



Clone 5C11

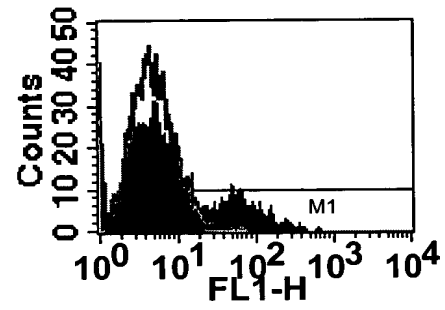


Figure 4B

CM1 (5.36×10^{-8} M)

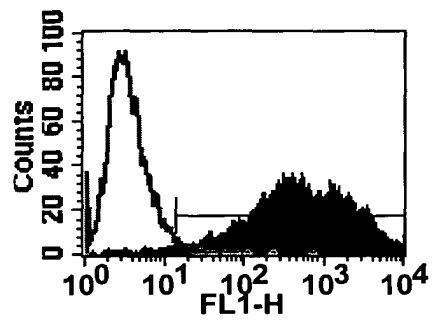
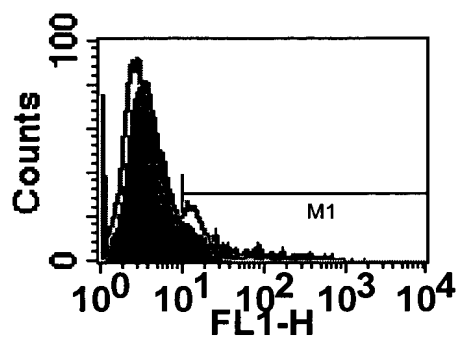
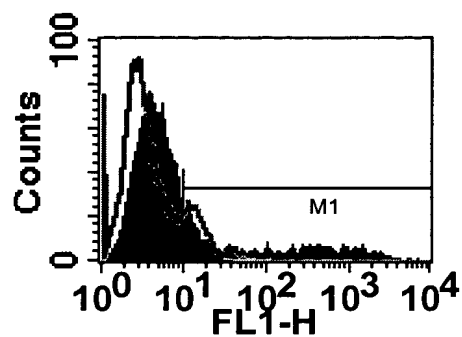


Figure 5A

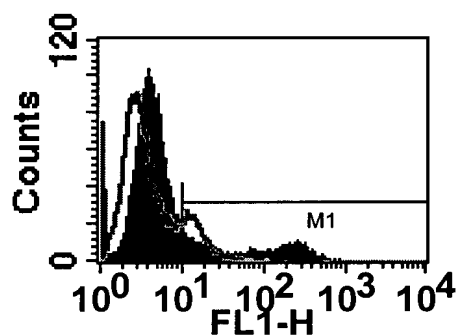
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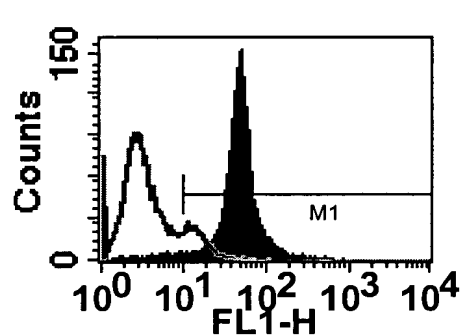
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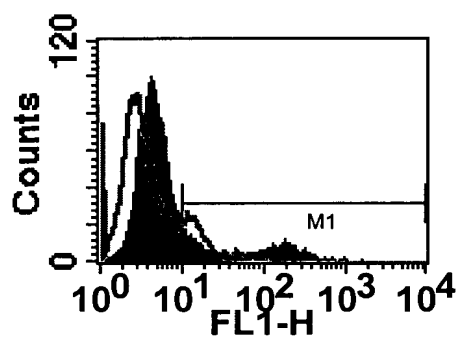
Clone 2F4



Clone 3B9



Clone 4E2



Clone 4F8

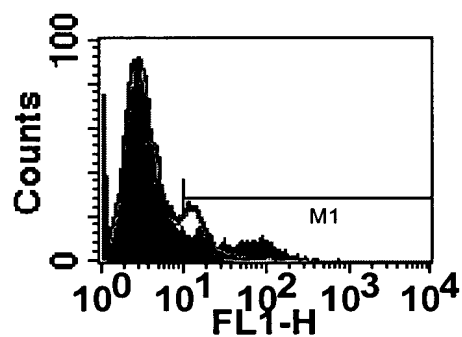
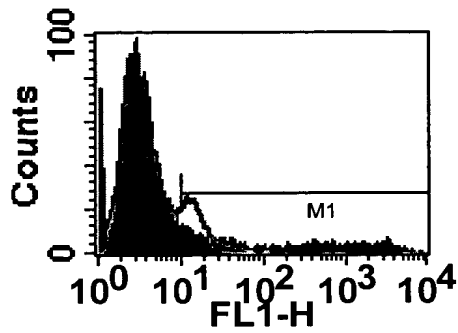
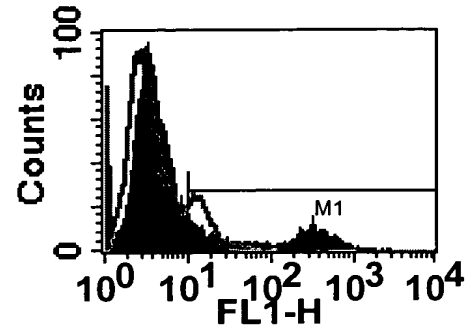


Figure 5A (continued)

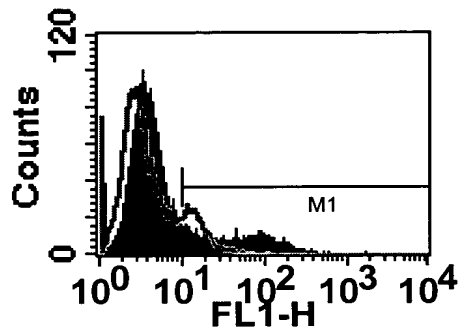
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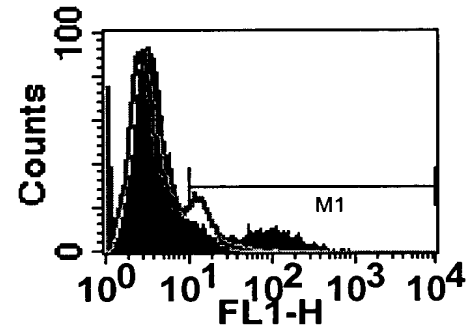
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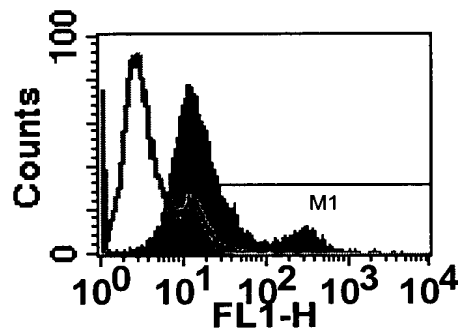
Clone 9E2



Clone 9G10



Clone 10C3



Clone 10G2

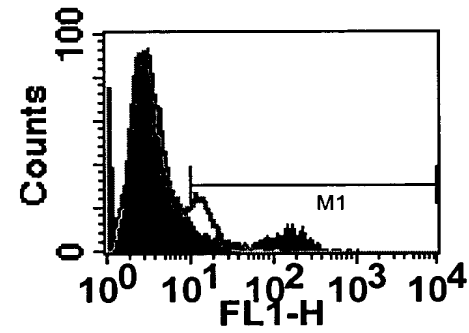
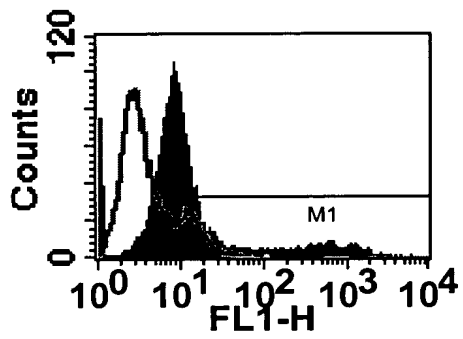
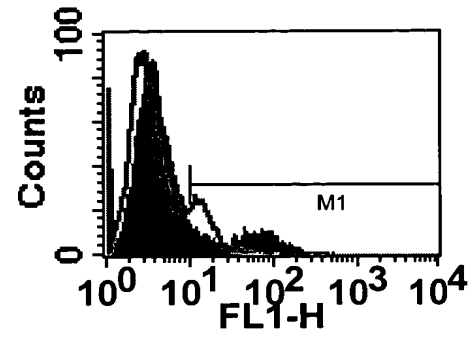


Figure 5A (continued)

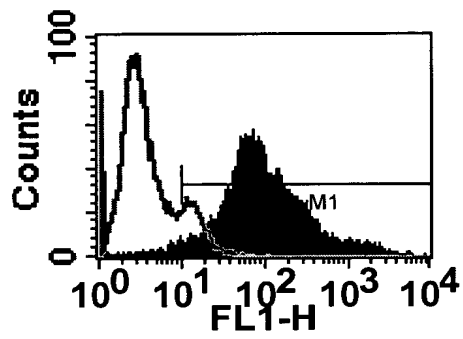
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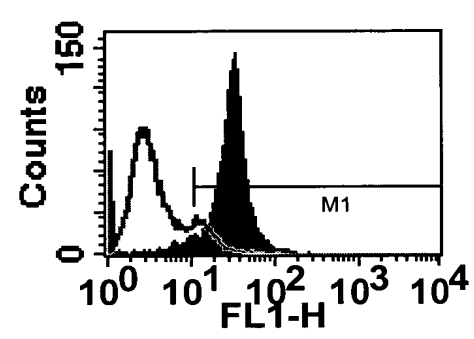
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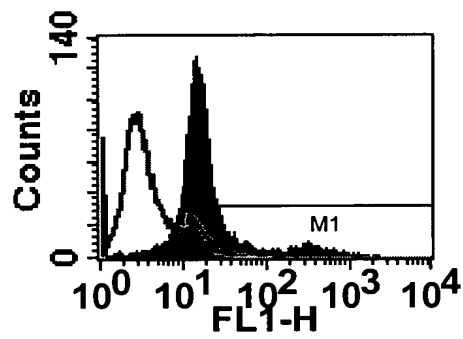
Clone 2F9



Clone 3C2



Clone 3E7



Clone 5C5

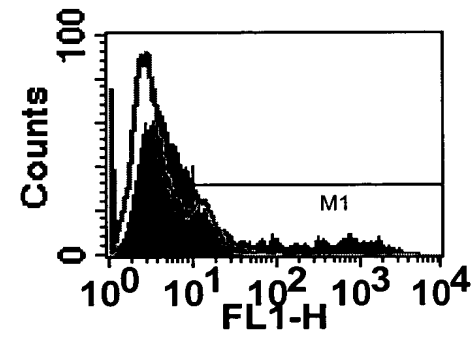
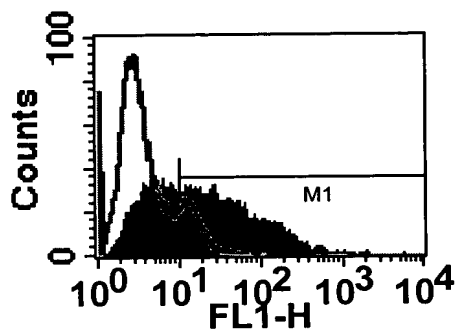
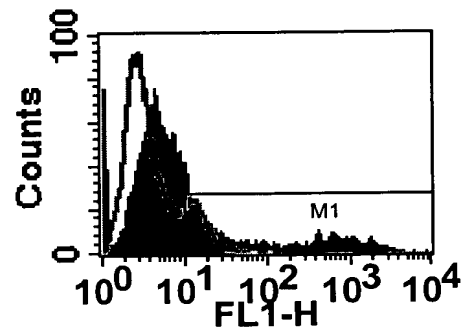


Figure 5A (continued)

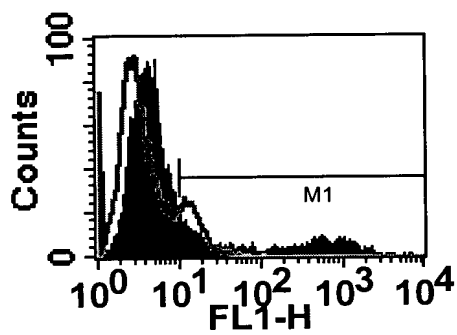
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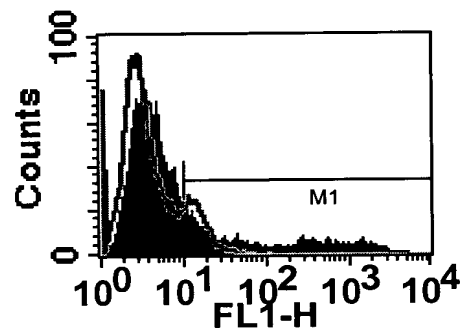
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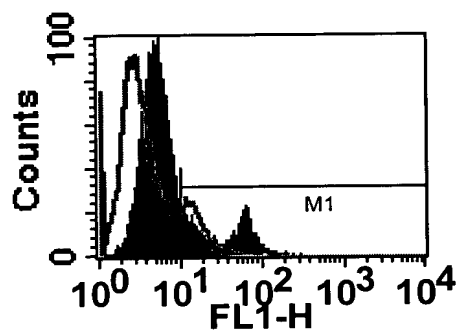
Clone 9D8



Clone 10C9



Clone 2D3



Clone 9G4

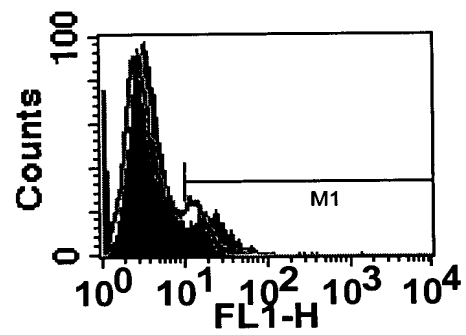


Figure 5B

M11

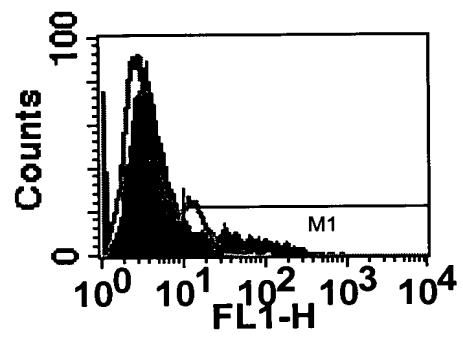


Figure 6A

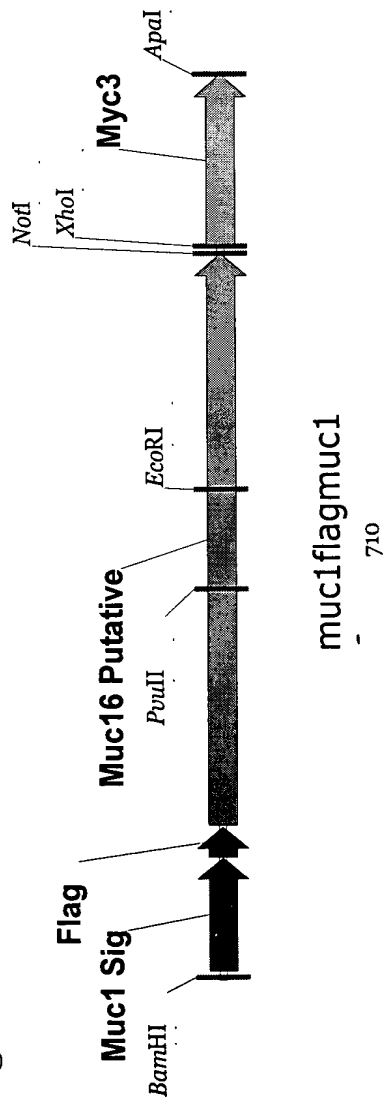


Figure 6B (SEQ ID NO:21)

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GGATCCATGA CACGGGCAC CCAGTCTCCT TTCTTCCTGC TGCTGCTCCT CACAGTGTCTT ACAGTTGTTA CAGGTTCTGG TCATGCAAGC TCTACCGACT ACAAGGACGA
CCTAGGTACT GTGCCCCGTG GGTGAGAGGA AAGAAGACG ACGACGAGGA GTGTCAACAA TGTCAACAAT GTCCAGACC AGTACGTTCC AGATGGCTGA TGTTCTCTGCT

111
CGATGACAG TCTAGATTCC GAAACAGCAG CATCAAGAGT TAATTTCTG ACTGTCAAGT TTCAACATTG AGGTCTGTCC CCAACAGGCA CCACACCGGG GTGGACTCCC
GCTACTGTT AGATCTAAG CTTTGTCTG GTAGTTCTCA ATAAAAAGAC TGACAGTTCA AAGTTGTAA TCCAGACAGG GGTGTCTCCT GGTGTGGCCC CACCTGAGGG

221
TGTTGTAATT CTGCCCCAG GCTCGGAGG TAGACAGAGT TGCCATCTAT GAGGAATTC TGCGGATGAC CCGGATGCT ACCCAGCTGC AGAATTTAC CCTGGACAGG
ACACATTGAA GAGCGGTGAC CGAGCCTCTC ATCTGTCTCA ACGGTAGATA CTCCTTAAAG ACGCTACTG GGCCTTACCA TGGGTGACG TCTTGAAAGT GGCCTGTCC

331
AGCAGTGTCC TTGTGGATGG GTATTCTCCC AACAGAAATG AGCCCTTAAC TGGGAATTC GACCTTCCCT TCTGGGCTGT CATCCTCATC GGCTTGGCAG GACTCCTGGG
TCGTACAGG AACACCTACC CATAGAGGG TTGTCTTTAC TCGGGAATG ACCCTTAAGA CTGGAAGGGA AGACCCGACA GTAGGAGTAG CCGAACCCTC CTGAGGACCC

441
ACTCATACA TGCCTGATCT GCGGTGCTCT GGTGACCACC CGCCGGCGGA AGAAGGAAGG AGAATACAAC GTCCAGCAAC AGTGCCGAGG CTACTACCCAG TCACACCTAG
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551
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661
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Figure 7

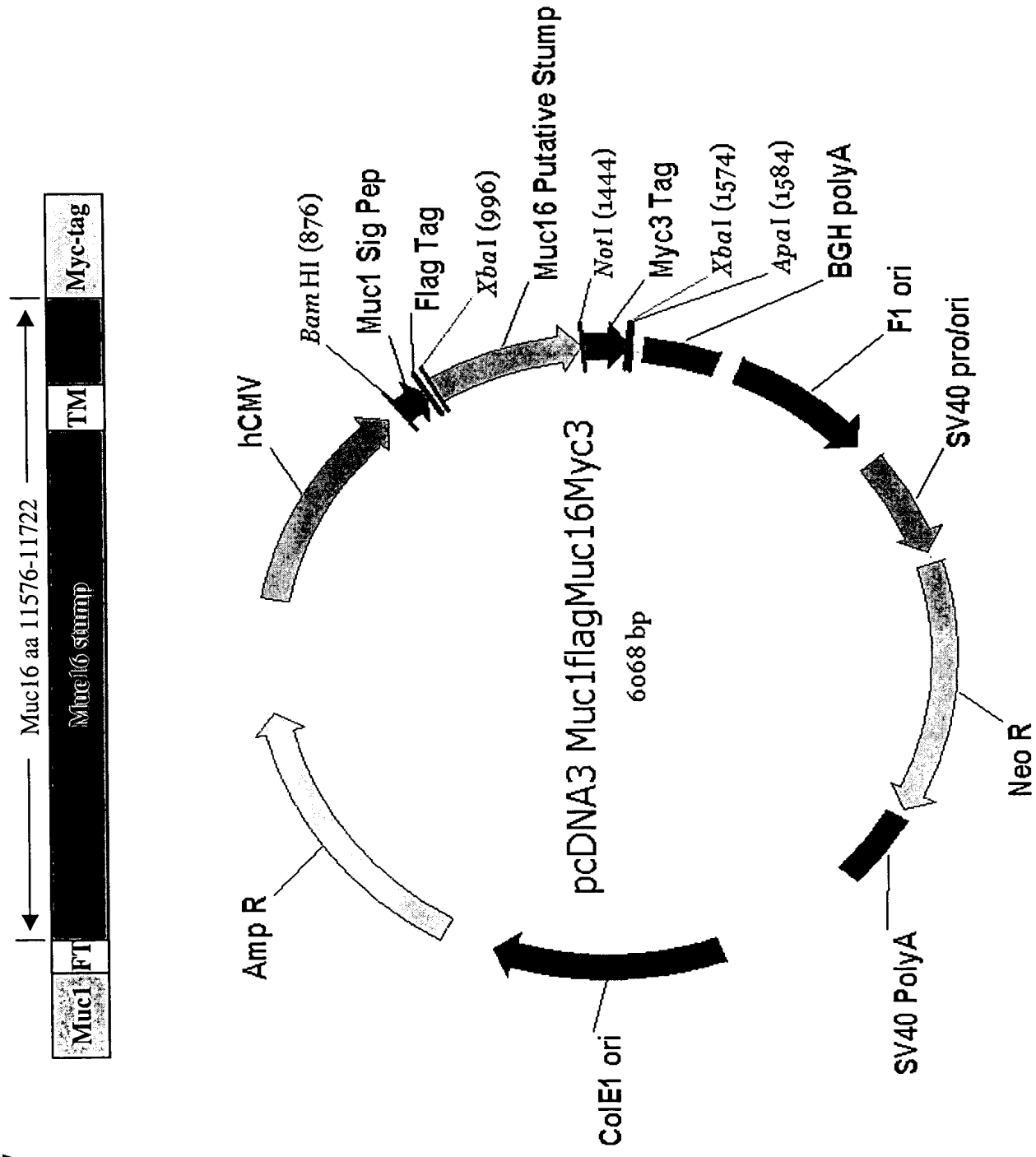


Figure 8

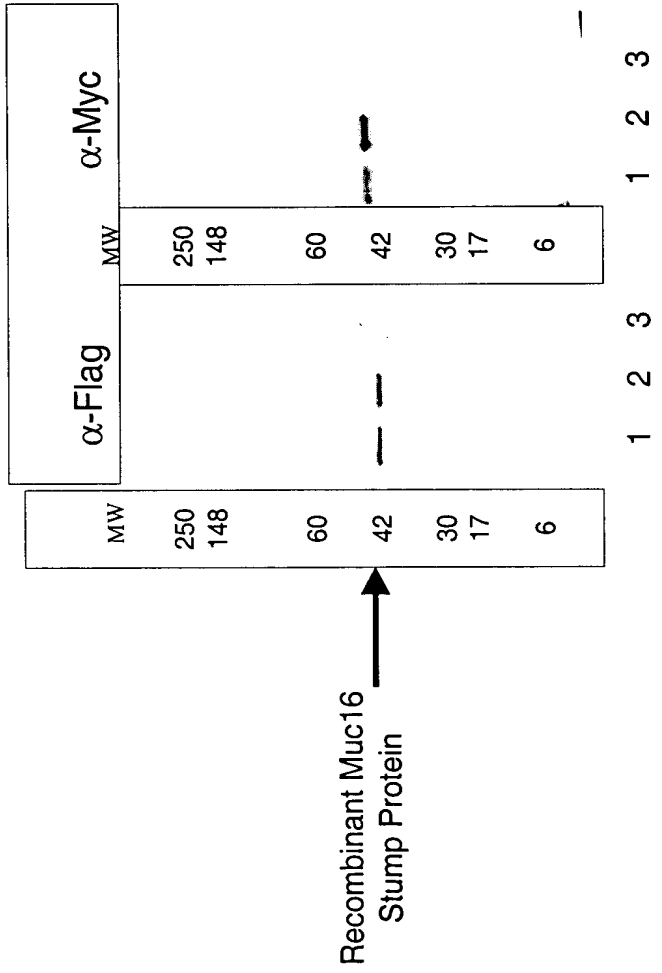


Figure 9

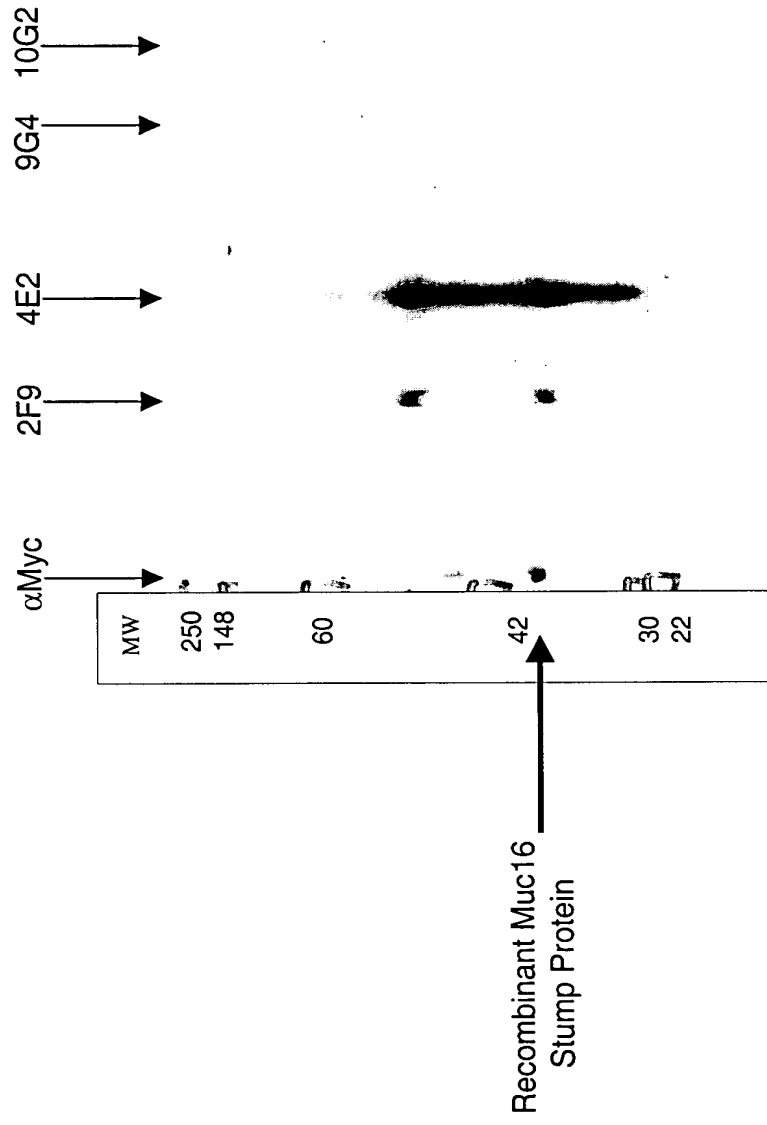


Figure 10A

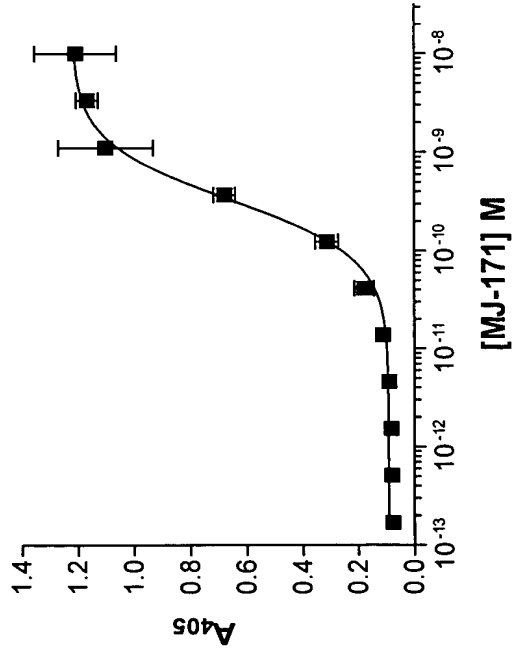


Figure 10B

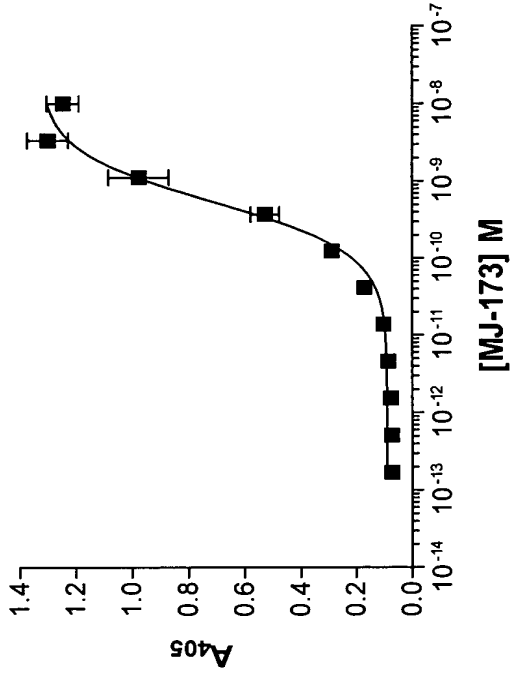
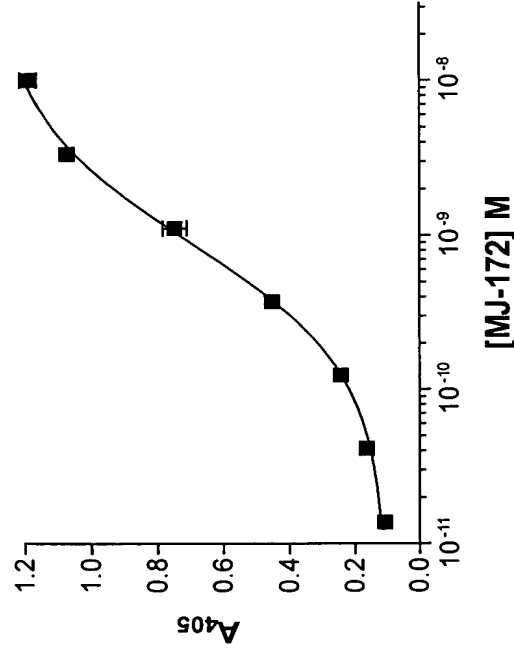


Figure 10C



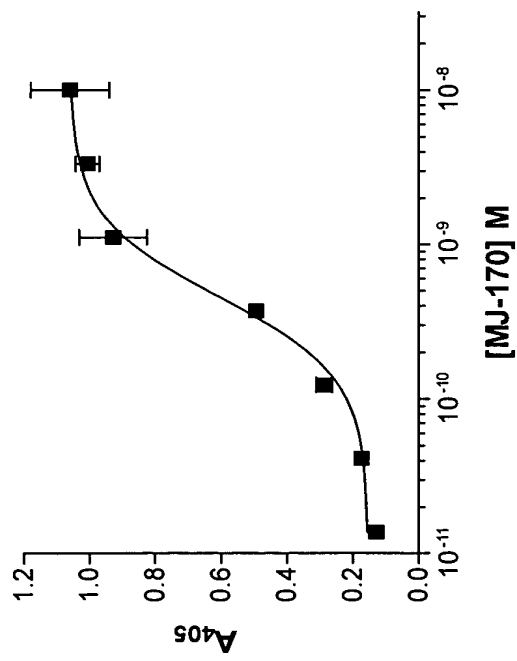


Figure 11

Figure 12A

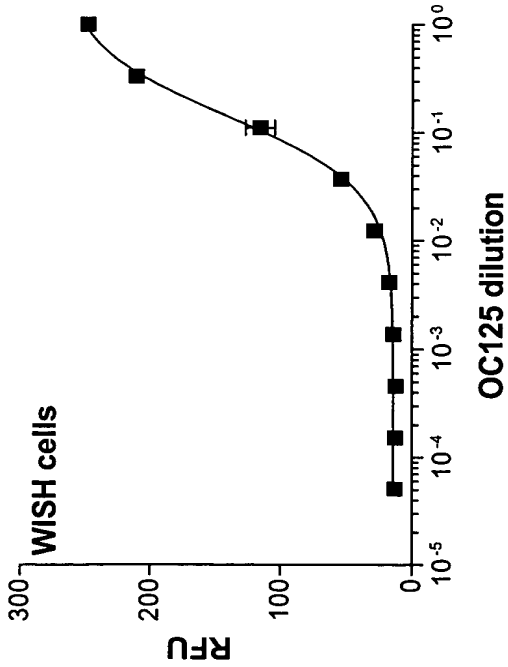


Figure 12B

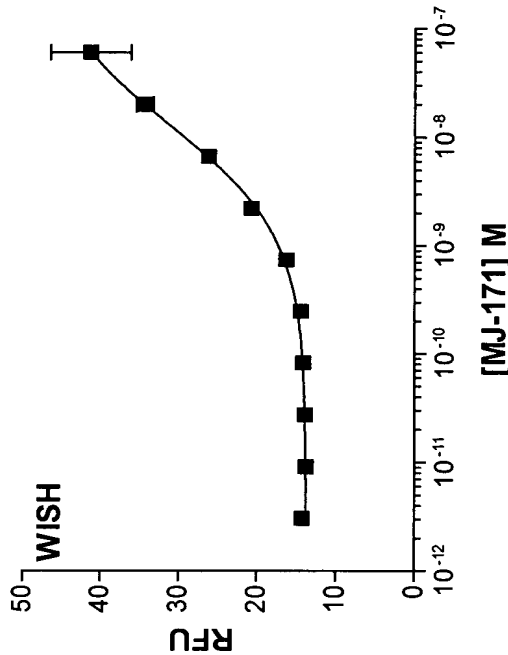


Figure 12C

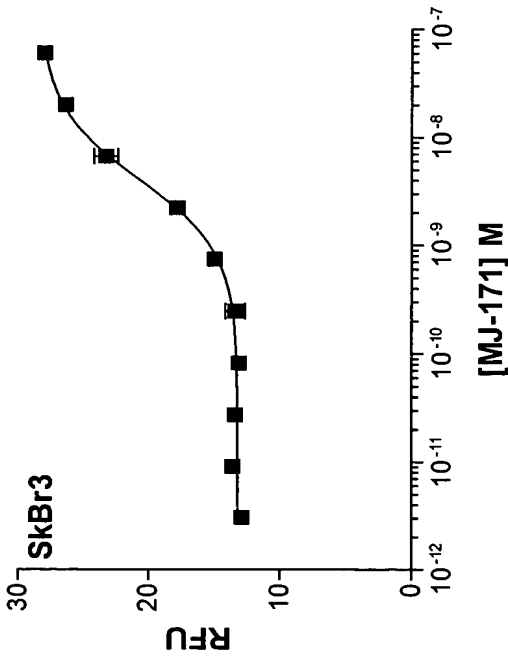


Figure 12D

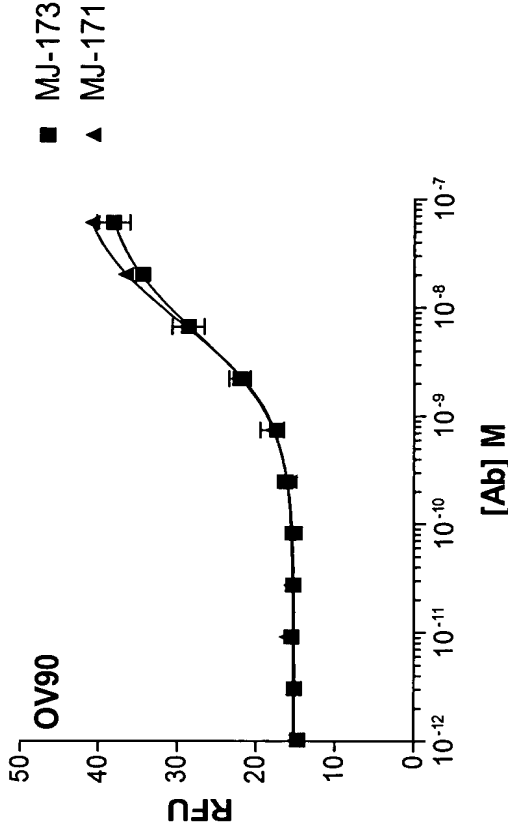


Figure 12E

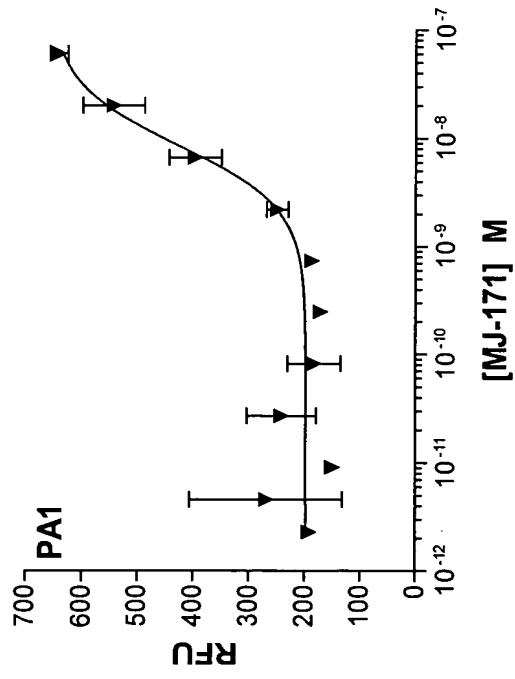


Figure 12G

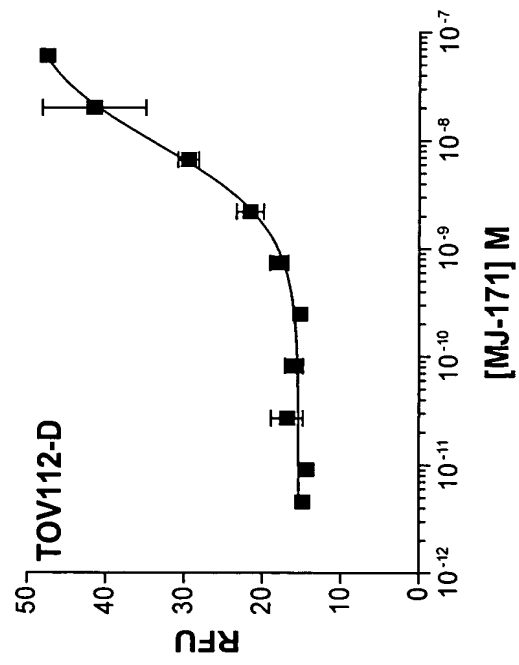


Figure 12F

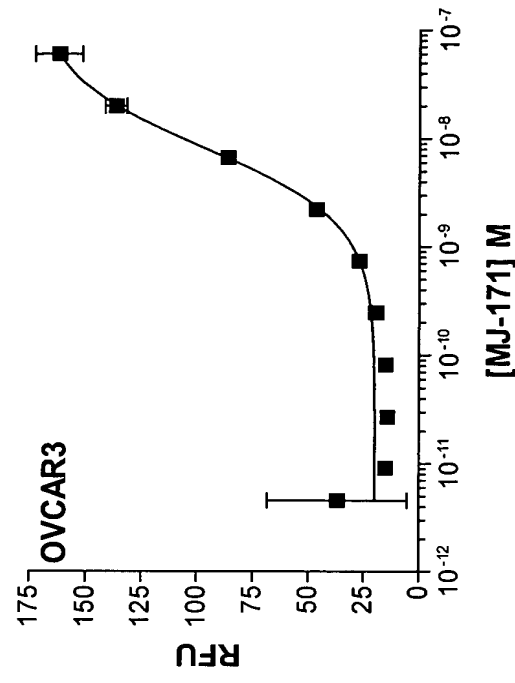


Figure 13A

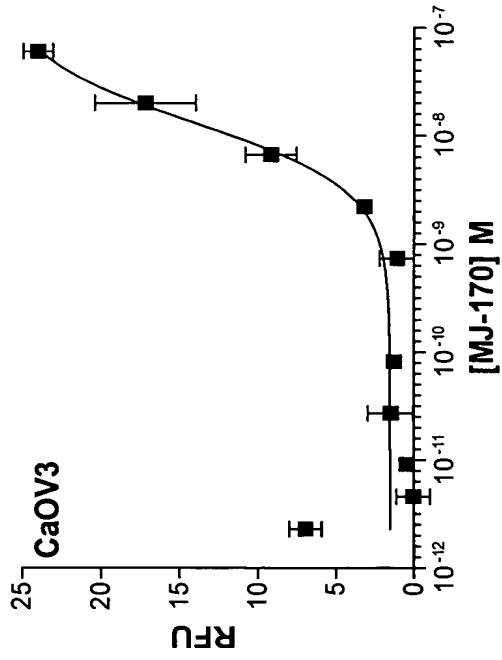


Figure 13B

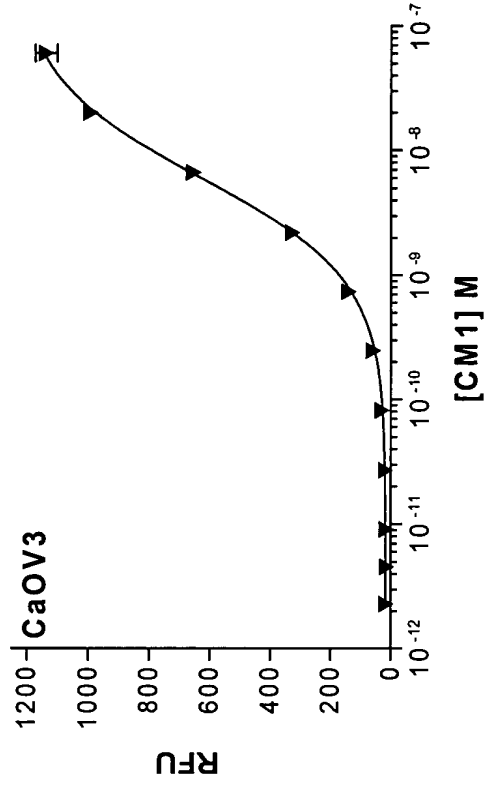


Figure 14A

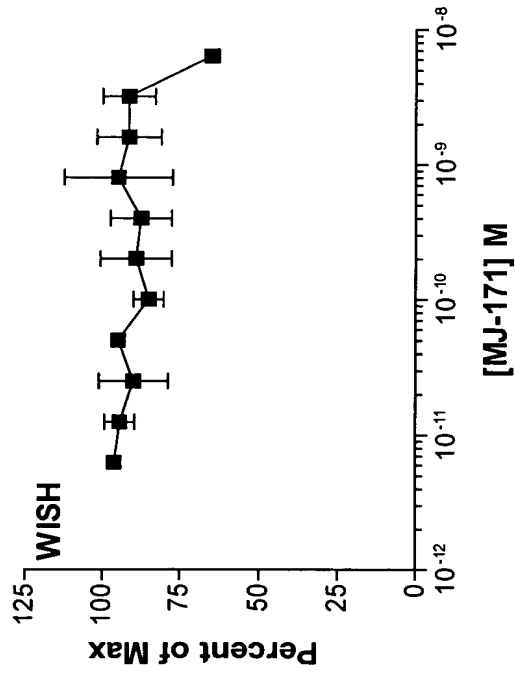


Figure 14B

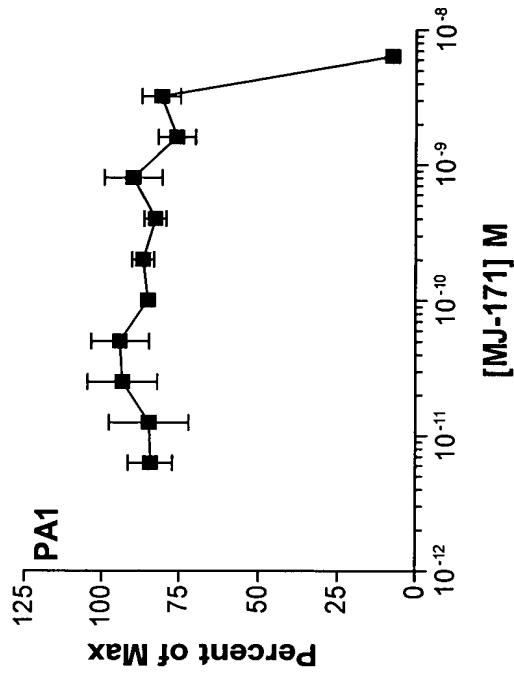


Figure 14C

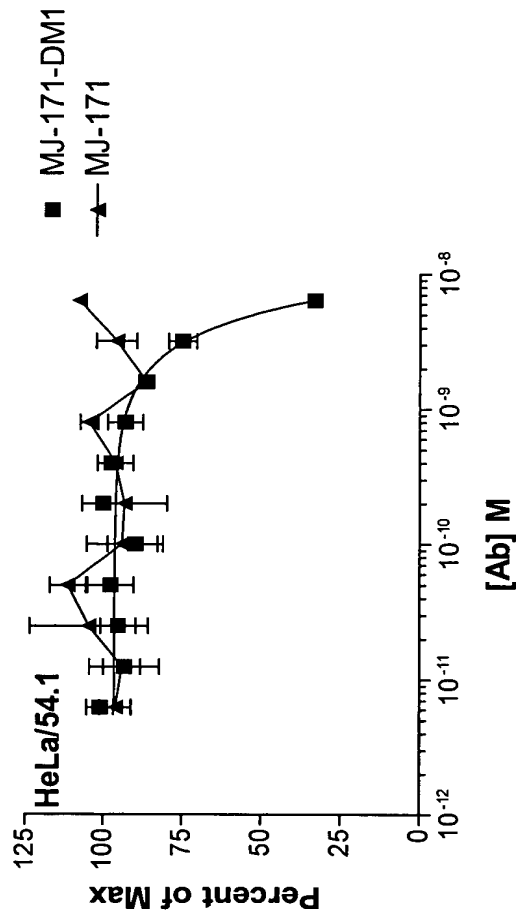


Figure 15

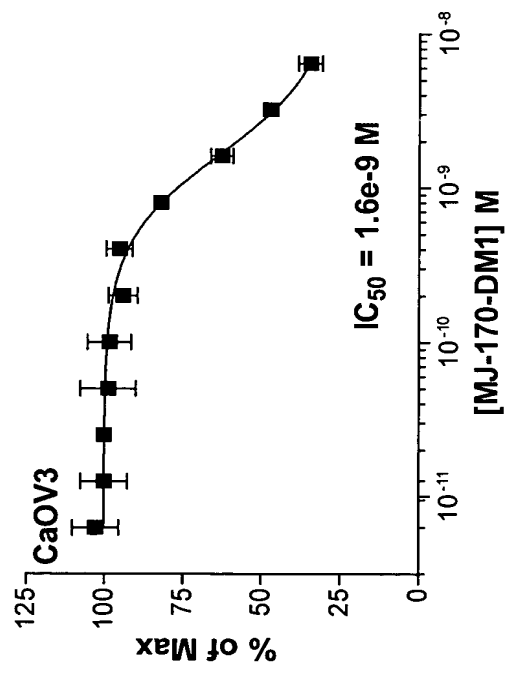


Figure 16

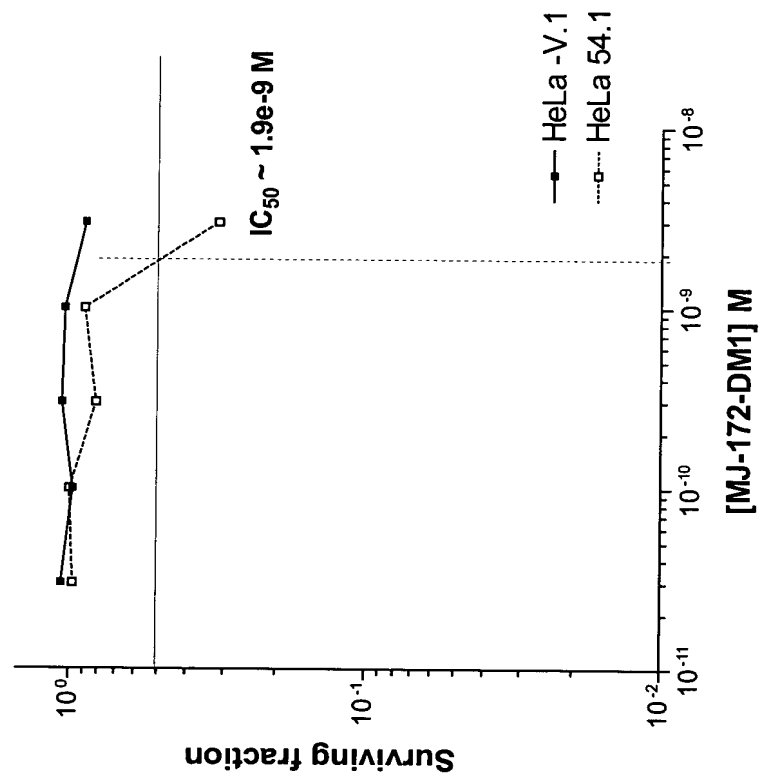


Figure 17

